

Metabolomics symposium highlights the field's triumphs and challenges

By Heather Franco

Wouldn't it be easier to fish using explosives instead of a hook and line? Keynote speaker Ian Wilson, Ph.D., of the [Imperial College London](http://www3.imperial.ac.uk/), used that very metaphor to describe large-scale omics searches for early biomarkers of disease, at the start of the Aug. 9 symposium on metabolomics platforms.

"People call metabolomics fishing," Wilson joked, "but I say that I fish with hand grenades."

In her opening comments, [Susan Sumner, Ph.D.](http://www.rti.org/newsroom/experts.cfm?obj=1958B5A7-73A2-4C7B-B3502AB6EB5F5AB3), organizer and host of the National Institutes of Health (NIH) Eastern Regional Comprehensive Metabolomics Resource Core (RCMRC) Symposium at RTI International headquarters in Research Triangle Park, N.C., offered a more straightforward definition for the audience, which included a number of scientists from NIEHS.

"Metabolomics involves the broad-spectrum analysis of the low molecular weight complement of cells, tissues, and biological fluids," explained Sumner, who is director of the [RTI RCMRC](http://www.rti.org/page.cfm/Metabolomics_Research). "It allows us to determine the pattern of changes in the related metabolites arising from any disease, dysfunction, disorder, or exposure."

A love-hate relationship with metabolic analysis platforms

Wilson gave a rousing address on "How NOT to do Metabolic Profiling," with a focus on the metabolic techniques that he has used for years. He described his experiences with nuclear magnetic resonance (NMR) and liquid chromatography-mass spectrometry (LC-MS).

"NMR is like a mother that is reliable and doesn't lie to you, but is often insensitive," he joked. "LC-MS is like a lover that lies to you." According to Wilson, the trick is to turn LC-MS into a trusted partner, through the use of quality controls.

Despite its drawbacks, Wilson believes LC-MS can be an efficient and sensitive technique. As he explained with yet another attention-getting metaphor, "LC-MS includes everything, which means you see everything. Thus, the challenge is to take oceans of data, and make rivers of information, and finally puddles of knowledge."

NIH program supports the development of metabolomics

The RTI RCMRC is one of three cores funded by the [NIH Common Fund](http://commonfund.nih.gov/Metabolomics/index.aspx), to establish national standards, increase the national capacity to provide metabolic profiling and data analysis, and facilitate institutional development of research, training, and outreach.

Sumner described the RTI core's pilot and feasibility study program, highlighting research performed with Richard Loesser, M.D., of Wake Forest University, to determine biomarkers important in development and progression of osteoarthritis. Sumner also described the RTI core's internship program, and the NIH funded metabolomics training programs at the University of North Carolina at Chapel Hill directed by Martin Kohlmeier, M.D., and University of Alabama at Birmingham with Stephen Barnes, Ph.D.

In a second talk about work at the RTI core, [James Raymer, Ph.D.](http://www.rti.org/page.cfm?objectid=9C903D09-65A4-4612-8DE9AACD22D9836B), an analytical chemist, described the development and use of gas chromatography-mass spectrometry (GC-MS) in metabolic profiling for environmental health studies (see [text box](#)).

The daylong program also included talks by scientists from industry groups about the use of two-dimensional gas



Sumner described the metabolic profiling program that she oversees as part of the [RTI RCMRC Pilot and Feasibility Program](http://www.rti.org/files/RTI%20RCMRC%20Call%20for%20Applications.pdf). The program requires recipients of pilot and feasibility grants to make their data publicly available. (Photo courtesy of Steve McCaw)



With his dry wit and often self-deprecating humor, keynote speaker Wilson kept everyone in the audience laughing, as he described his triumphs and failures in metabolic research over the years. (Photo courtesy of Steve McCaw)

chromatography-mass spectrometry (GCxGC-MS) and the applications of metabolomics in agricultural research.

Symposium opens avenues for NIEHS scientists

NIEHS scientists attended the symposium to learn about metabolomics and how to apply it to their research. As Environmental Genomics Group fellow [Mehmet Karaca, Ph.D.](#), explained, "The symposium made me appreciate how using proper metabolomics analysis, it is possible to catch the differences in seemingly similar biological samples." [Honglei Chen, M.D., Ph.D.](#), lead researcher and head of the Aging and Neuroepidemiology Group, said, "I found the discussions about technology and quality control very useful."

Thus, the symposium achieved its goal of facilitating future metabolomic studies. As [Carl Bortner, Ph.D.](#), director of the NIEHS Flow Cytometry Center, observed, "It is clear to me that as this technology continues to move forward and becomes more advanced, the detection of metabolites in many different types of samples will lead to great discoveries in science."

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The symposium highlighted the many challenges that metabolic profilers face. As [Leesa Deterding, Ph.D.](#), left, director of the NIEHS Collaborative Mass Spectrometry Support Group, explained, "In biomarker discovery, the difficulty is in discovering and identifying a compound that is relevant to the biological question." (Photo courtesy of Steve McCaw)



Jack Cochran, from chromatography manufacturer Restek, delivered an informative lecture on the development and applicability of GCxGC-MS in metabolomics. (Photo courtesy of Steve McCaw)



Raymer described how his group at RTI is utilizing GC-MS to study ecometabolomics, with direct applications for environmental health science research. (Photo courtesy of Steve McCaw)

Ecometabolism - new directions in toxicology research?

At the RTI RCMRC, Raymer and colleagues are using metabolic profiling to discern changes in metabolites in various disease and exposure models, termed ecometabolomics. They are currently working on three projects and hope to collaborate with additional environmental scientists.

Effect of climate change on mayfly metabolism

In collaboration with [David Buchwalter, Ph.D.](http://tox.sciences.ncsu.edu/people/david-b-buchwalter/),
(<http://tox.sciences.ncsu.edu/people/david-b-buchwalter/>)
at North Carolina State University, Raymer subjected mayflies to hypoxia and heat challenges. GC-MS analysis was able to separate the groups and identify metabolites potentially involved in adaptive responses.

Using exhaled breath to study respiratory disease

Using an RTube, vapors and aerosolized drops from exhaled breath were condensed for GC-MS analysis. Samples have been collected from patients with asthma, chronic obstructive pulmonary disease, and cystic fibrosis, and are being analyzed for comprehensive discovery investigation.

Analyzing the impact of particulate matter on human health

Particulate matter (PM) represents a public health concern, as it has been linked to asthma and cardiovascular disease. Currently, two projects are underway using GC-MS to assess the impact of PM exposure on human health. One study assesses the effect of wood smoke exposure on the development of asthma in children. The other determines the impact of PM exposure in a controlled chamber in adults.

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